

IUBMB Enzyme Nomenclature**EC 3.3.2.6**

Common name: leukotriene-A₄ hydrolase

Reaction: (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicosa-7,9,11,14-tetraenoate + H₂O = (6Z,8E,10E,14Z)-(5S,12R)-5,12-dihydroxyicosa-6,8,10,14-tetraenoate

Other name(s): LTA₄ hydrolase; LTA4H

Systematic name: (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicosa-7,9,11,14-tetraenoate hydrolase

Comments: Converts 4,5-leukotriene A₄ into leukotriene B₄. Highly specific. Not identical with EC 3.3.2.3 epoxide hydrolase.

Links to other databases: [BRENDA](#), [EXPASY](#), [KEGG](#), [ERGO](#), [PDB](#), CAS registry number: 90119-07-6

References:

1. Evans, J.F., Dupuis, P. and Ford-Hutchinson, A.W. Purification and characterisation of leukotriene A₄ hydrolase from rat neutrophils. *Biochim. Biophys. Acta* 840 (1985) 43-50. [Medline UI: [85200023](#)]
2. Minami, M., Ohno, S., Kawasaki, H., Rådmark, O., Samuelsson, B., Jörnvall, H., Shimizu, T., Seyama, Y. and Suzuki, K. Molecular cloning of a cDNA coding for human leukotriene A₄ hydrolase - complete primary structure of an enzyme involved in eicosanoid synthesis. *J. Biol. Chem.* 262 (1987) 13873-13876.

[EC 3.3.2.6 created 1989]

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 1HS6**STRUCTURE OF LEUKOTRIENE A4 HYDROLASE COMPLEXED WITH BESTATIN.**

Chains A
E Value 0.0
Characteristics Deposited: 24-Dec-2000 Exp. Method: X Ray Diffraction
Resolution: 1.95 Å
Classification Hydrolase
Compound Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase
Authors Thunnissen, M.M., Nordlund, P., Haeggstrom, J.Z.
Alignment stats Length: 610 Score: 1222.99bits (3163) E-value: 0.0 Identities: 610/610 (100%) Positives: 610/610 (100%) Gaps: 0/610 (0%)

Alignment

1	10	20	30	40	50	60
Query PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						
PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						

 1H19**STRUCTURE OF [E271Q] LEUKOTRIENE A4 HYDROLASE**

Chains A
E Value 0.0
Characteristics Deposited: 04-Jul-2002 Exp. Method: X Ray Diffraction
Resolution: 2.10 Å
Classification Hydrolase
Compound Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: YES
Authors Rudberg, P.C., Tholander, F., Thunnissen, M.M., Haeggstrom, J.Z.
Alignment stats Length: 610 Score: 1221.84bits (3160) E-value: 0.0 Identities: 609/610 (100%) Positives: 610/610 (100%) Gaps: 0/610 (0%)

Alignment

1	10	20	30	40	50	60
Query PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						
PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						
Sbjct PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						

1GW6

**STRUCTURE OF LEUKOTRIENE A4 HYDROLASE D375N MUTANT**

Chains A
E Value 0.0
Characteristics Deposited: 07-Mar-2002 Exp. Method: X Ray Diffraction
Resolution: 2.20 Å
Classification Hydrolase
Compound Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: YES
Authors Rudberg, P., Tholander, F., Thunnissen, M., Samuelsson, B., Haeggstrom, J.
Alignment stats Length: 610 Score: 1221.07bits (3158) E-value: 0.0 Identities: 609/610 (100%) Positives: 610/610 (100%) Gaps: 0/610 (0%)

Alignment

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Query PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						
PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						
Sbjct PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLGTAAALTVQSQEDNRLSVLVDTKDLTIEKVVI						

1SQM

**STRUCTURE OF [R563A] LEUKOTRIENE A4 HYDROLASE**

Chains A
E Value 0.0
Characteristics Deposited: 19-Mar-2004 Exp. Method: X Ray Diffraction
Resolution: 2.30 Å
Classification Hydrolase
Compound Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: R563A
Authors Rudberg, P.C., Tholander, F.O.T., Andberg, M., Thunnissen, M.M.G.M.
Alignment stats Length: 610 Score: 1220.68bits (3157) E-value: 0.0 Identities: 609/610 (100%) Positives: 609/610 (100%) Gaps: 0/610 (0%)

Alignment

	1	10	20	30	40	50	60
Query	PEIVDTCSLASPASVCR	TKHLHRLCSVDPT	RTTLTGTAALT	TVQSQEDNLRSLVLD	LTKDLTIEK	VVI	
Sbjct	PEIVDTCSLASPASVCR	TKHLHRLCSVDPT	RTTLTGTAALT	TVQSQEDNLRSLVLD	LTKDLTIEK	VVI	

 1Z1W**Crystal structures of the tricorn interacting factor F3 from Thermoplasma acidophilum, a zinc aminopeptidase in three different conformations****Chains**

A

E Value

4.07144E-20

Characteristics

Deposited: 07-Mar-2005 Exp. Method: X Ray Diffraction

Classification

Resolution: 2.70 Å

Compound

Hydrolase

Authors

Mol. Id: 1 Molecule: Tricorn Protease Interacting Factor F3

Kyrieleis, O.J.P., Goettig, P., Kiefersauer, R., Huber, R., Brandstetter, H.

Alignment stats

Length: 426 Score: 95.9005bits (237) E-value: 4.07144E-20 Identities: 108/426 (25%)

Positives: 177/426 (42%) Gaps: 57/426 (13%)

Alignment

	52	60	70	80	90	100	110
Query	VLDTKDLTIEKV	WNGV	EVYALGEROSYKGSPW	PLISPLIALSKNQEIV	IEISFETSPKSSAL	W	
Sbjct	VLDAVGLGIVNW	KVNGV	ITAT	YGDGT	APGQ	QMRIEISPAGYUS	

 1Z5H**Crystal structures of the Tricorn interacting Factor F3 from Thermoplasma acidophilum****Chains**

A,B

E Value

4.07144E-20

Characteristics

Deposited: 18-Mar-2005 Exp. Method: X Ray Diffraction

Classification

Resolution: 2.30 Å

Compound

Hydrolase

Authors

Mol. Id: 1 Molecule: Tricorn Protease Interacting Factor F3

Kyrieleis, O.J.P., Goettig, P., Kiefersauer, R., Huber, R., Brandstetter, H.

Alignment stats

Length: 426 Score: 95.9005bits (237) E-value: 4.07144E-20 Identities: 108/426 (25%)

Positives: 177/426 (42%) Gaps: 57/426 (13%)

Alignment

	52	60	70	80	90	100	110
Query	VLDTKDLTIEKV	WNGV	EVYALGEROSYKGSPW	PLISPLIALSKNQEIV	IEISFETSPKSSAL	W	
Sbjct	VLDAVGLGIVNW	KVNGV	ITAT	YGDGT	APGQ	QMRIEISPAGYUS	

 2GTQ**Crystal structure of aminopeptidase N from human pathogen N. meningitidis****Chains**

A

E Value

1.35851E-7

Characteristics

Deposited: 28-Apr-2006 Exp. Method: X Ray Diffraction

Classification

Resolution: 2.05 Å

Compound

Hydrolase

Authors

Mol. Id: 1 Molecule: Aminopeptidase N

Nocek, B., Muligan, R., Bargassa, M., Joachimiak, A.

Alignment stats

Length: 481 Score: 54.299bits (129) E-value: 1.35851E-7 Identities: 111/481 (23%)

Positives: 170/481 (35%) Gaps: 61/481 (13%)

Alignment

	52	60	70	80	90	100	110
Query	LVLDTKDLTIEKV	WNGV	EVYALGEROSYKGSPW	PLISPLIALSKNQEIV	IEISFETSPKSSAL	W	
Sbjct	LVLD	V ING	Y L GE	G P E	-E- E P		

 1NNJ**Crystal structure Complex between the Lactococcus lactis Fpg and an abasic site containing DNA****Chains**

A

E Value

2.10075

Characteristics

Deposited: 14-Jan-2003 Exp. Method: X Ray Diffraction

Classification

Resolution: 1.90 Å

Compound

Hydrolase

Authors

Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase Mutation: P1G

Serre, L., Pereira de Jesus, K., Boiteux, S., Zelwer, C., Castaing, B.

Alignment stats

Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85

(49%) Gaps: 13/85 (15%)

Alignment	281	290	300	310	320	330	340
Query	T	L	A	G	D	K	S
TL	AG	L	N	E	W	-	K
Sbjct	TL	AG	--L	N	Y	V	E

164 170 180 190 200 210 220

 1PJI

Crystal structure of wild type Lactococcus lactis FPG complexed to a 1,3-propanediol containing DNA

Chains

A

E Value

2.10075

Characteristics

Deposited: 03-Jun-2003 Exp. Method: X Ray Diffraction

Resolution: 1.90 Å

Classification

Hydrolase/dna

Compound

Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase

Authors

Pereira, K., Serre, L., Zelwer, C., Castaing, B.

Alignment stats

Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

 Alignment

	281	290	300	310	320	330	340
Query	T	L	A	G	D	K	S
TL	AG	L	N	E	W	-	K
Sbjct	TL	AG	--L	N	Y	V	E

164 170 180 190 200 210 220

 1PJJ

Complex between the Lactococcus lactis Fpg and an abasic site containing DNA.

Chains

A

E Value

2.10075

Characteristics

Deposited: 03-Jun-2003 Exp. Method: X Ray Diffraction

Resolution: 1.90 Å

Classification

Hydrolase/dna

Compound

Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase Mutation: P1G

Authors

Serre, L., Pereira de Jesus, K., Boiteux, S., Zelwer, C., Castaing, B.

Alignment stats

Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

 Alignment

	281	290	300	310	320	330	340
Query	T	L	A	G	D	K	S
TL	AG	L	N	E	W	-	K
Sbjct	TL	AG	--L	N	Y	V	E

164 170 180 190 200 210 220

12 ◀

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:50:03 ; Search time 189 Seconds
(without alignments)
1418.101 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.....HKASMHPVTAMLVKGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query						Description
No.	Score	Match	Length	DB	ID		

1	3225	100.0	611	3	AAB08840		Aab08840 Amino aci
2	3225	100.0	611	8	ABM81460		Abm81460 Tumour-as
3	3225	100.0	611	9	ADW07254		Adw07254 Human hep
4	3225	100.0	611	9	ADZ04287		Adz04287 Human leu
5	3222	99.9	611	7	ADE25724		Ade25724 Human pro
6	3042.5	94.3	610	8	ADT66633		Adt66633 Rat leuko
7	2963	91.9	625	3	AAB58111		Aab58111 Lung canc
8	2696	83.6	532	8	ADL99491		Adl99491 Human leu

9	2438.5	75.6	480	8	ADL99494	Adl99494 Human leu
10	1464	45.4	587	8	ADN23312	Adn23312 Bacterial
11	1376.5	42.7	809	8	ADN23545	Adn23545 Bacterial
12	1338	41.5	613	4	ABB71965	Abb71965 Drosophil
13	1206.5	37.4	612	8	ADS44280	Ads44280 Bacterial
14	1134.5	35.2	671	6	ABR52866	Abr52866 Protein s
15	1134.5	35.2	671	7	ADK62338	Adk62338 Disease t
16	1134.5	35.2	671	8	ADN19334	Adn19334 Bacterial
17	1079	33.5	694	8	ADN21345	Adn21345 Bacterial
18	1059.5	32.9	623	2	AAW02284	Aaw02284 Candida a
19	1030.5	32.0	573	8	ADS30208	Ads30208 Bacterial
20	1018.5	31.6	584	9	ABM96671	Abm96671 M. xanthu
21	1006.5	31.2	650	5	AAU72906	Aau72906 Human met
22	1006.5	31.2	650	5	ADR43717	Adr43717 Human pro
23	1006.5	31.2	650	6	ABP59205	Abp59205 Human ami
24	1006.5	31.2	650	7	ADD45336	Add45336 Human Pro
25	1006.5	31.2	650	8	ABM80228	Abm80228 Tumour-as
26	1006.5	31.2	658	7	ADC31289	Adc31289 Human nov
27	1005.5	31.2	650	4	AAB84214	Aab84214 Amino aci
28	1001.5	31.1	650	7	ADD45334	Add45334 Rat Prote
29	1000	31.0	657	8	ADR97314	Adr97314 Human RNP
30	987	30.6	626	7	ADM05614	Adm05614 Human pro
31	954	29.6	569	8	ADN26507	Adn26507 Bacterial
32	947	29.4	671	8	ADS28564	Ads28564 Bacterial
33	929.5	28.8	588	8	ADS27297	Ads27297 Bacterial
34	929.5	28.8	588	8	ADS26935	Ads26935 Bacterial
35	929.5	28.8	641	8	ADS26559	Ads26559 Bacterial
36	887.5	27.5	650	8	ADY05243	Ady05243 Plant ful
37	880	27.3	540	8	ADN26764	Adn26764 Bacterial
38	874	27.1	581	8	ADS28769	Ads28769 Bacterial
39	800.5	24.8	724	5	AAU72907	Aau72907 Human met
40	800	24.8	725	5	ABB77908	Abb77908 Amino aci
41	800	24.8	725	8	ADL14157	Adl14157 Novel hum
42	766.5	23.8	416	4	AAM25679	Aam25679 Human pro
43	721	22.4	541	5	ADR41508	Adr41508 Human CD-
44	715.5	22.2	756	8	ADJ67633	Adj67633 Human ova
45	671.5	20.8	501	8	ADJ71950	Adj71950 Human PMM

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:03:01 ; Search time 47 Seconds
(without alignments)
1073.025 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.....HKASMHPVTAMLVKGDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
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1	2534	78.6	483	2 US-09-949-016-10002	Sequence 10002, A
2	1059.5	32.9	623	1 US-08-332-838-2	Sequence 2, Appli
3	1018.5	31.6	584	2 US-09-902-540-15870	Sequence 15870, A
4	1006.5	31.2	650	2 US-10-363-937-5	Sequence 5, Appli
5	1005.5	31.2	650	2 US-09-443-795-1	Sequence 1, Appli
6	840.5	26.1	362	2 US-09-270-767-43340	Sequence 43340, A
7	785.5	24.4	587	2 US-09-949-016-9933	Sequence 9933, Ap
8	783	24.3	429	2 US-09-248-796A-17980	Sequence 17980, A
9	557.5	17.3	285	2 US-09-270-767-42260	Sequence 42260, A
10	341	10.6	972	2 US-08-335-844A-23	Sequence 23, Appl
11	341	10.6	972	2 US-09-129-366-23	Sequence 23, Appl

12	340.5	10.6	1025	1	US-08-530-792D-23	Sequence 23, Appl
13	337	10.4	972	2	US-08-335-844A-24	Sequence 24, Appl
14	337	10.4	972	2	US-09-129-366-24	Sequence 24, Appl
15	330	10.2	1026	1	US-08-530-792D-22	Sequence 22, Appl
16	328	10.2	923	2	US-09-328-352-4371	Sequence 4371, Ap
17	324	10.0	919	2	US-09-919-039-222	Sequence 222, App
18	311	9.6	354	2	US-09-949-016-6929	Sequence 6929, Ap
19	304.5	9.4	990	2	US-10-363-937-7	Sequence 7, Appli
20	304	9.4	977	2	US-08-335-844A-22	Sequence 22, Appl
21	304	9.4	977	2	US-09-129-366-22	Sequence 22, Appl
22	298.5	9.3	957	2	US-09-949-016-6154	Sequence 6154, Ap
23	298.5	9.3	964	2	US-09-949-016-7431	Sequence 7431, Ap
24	298.5	9.3	967	2	US-09-139-802-201	Sequence 201, App
25	298.5	9.3	967	2	US-09-659-786-201	Sequence 201, App
26	297	9.2	850	2	US-09-902-540-10199	Sequence 10199, A
27	297	9.2	867	2	US-09-540-236-3193	Sequence 3193, Ap
28	296.5	9.2	699	2	US-09-270-767-45507	Sequence 45507, A
29	291.5	9.0	848	2	US-09-583-110-2738	Sequence 2738, Ap
30	290.5	9.0	912	2	US-09-902-540-16181	Sequence 16181, A
31	285	8.8	948	2	US-09-620-312D-1105	Sequence 1105, Ap
32	284	8.8	917	2	US-09-902-540-12845	Sequence 12845, A
33	281.5	8.7	941	2	US-09-991-181-353	Sequence 353, App
34	281.5	8.7	941	2	US-09-990-444-353	Sequence 353, App
35	281.5	8.7	941	2	US-09-997-333-353	Sequence 353, App
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37	273	8.5	874	2	US-09-489-039A-12124	Sequence 12124, A
38	264.5	8.2	815	2	US-09-107-433-5059	Sequence 5059, Ap
39	259.5	8.0	458	2	US-09-602-777A-124	Sequence 124, App
40	258	8.0	896	2	US-09-543-681A-7870	Sequence 7870, Ap
41	245.5	7.6	867	2	US-09-602-777A-104	Sequence 104, App
42	245	7.6	990	2	US-09-657-931A-11	Sequence 11, Appl
43	244.5	7.6	891	2	US-09-252-991A-28689	Sequence 28689, A
44	244.5	7.6	986	2	US-09-657-931A-12	Sequence 12, Appl
45	242	7.5	995	2	US-09-657-931A-1	Sequence 1, Appli

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:11:02 ; Search time 166 Seconds
(without alignments)
1535.397 Million cell updates/sec

Title: US-09-914-451-1

Perfect score: 3225

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	3225	100.0	611	5	US-10-873-595-6	Sequence 6, Appli
2	3222	99.9	611	4	US-10-247-671-128	Sequence 128, App
3	2963	91.9	625	3	US-09-925-302-449	Sequence 449, App
4	2963	91.9	625	3	US-09-925-302-449	Sequence 449, App
5	1464	45.4	587	4	US-10-369-493-5965	Sequence 5965, Ap
6	1376.5	42.7	809	4	US-10-369-493-6198	Sequence 6198, Ap
7	1338	41.5	613	6	US-11-097-143-42687	Sequence 42687, A
8	1206.5	37.4	612	4	US-10-369-493-22710	Sequence 22710, A
9	1134.5	35.2	671	4	US-10-369-493-1987	Sequence 1987, Ap
10	1079	33.5	694	4	US-10-369-493-3998	Sequence 3998, Ap
11	1030.5	32.0	573	4	US-10-369-493-19241	Sequence 19241, A

12	1006.5	31.2	650	4	US-10-363-937-5	Sequence 5, Appli
13	1006.5	31.2	650	4	US-10-275-107-66	Sequence 66, Appli
14	1006.5	31.2	650	6	US-11-167-040-5	Sequence 5, Appli
15	1005.5	31.2	650	3	US-09-854-875A-1	Sequence 1, Appli
16	1005.5	31.2	650	4	US-10-056-253-1	Sequence 1, Appli
17	1005.5	31.2	650	5	US-10-767-308-1	Sequence 1, Appli
18	987	30.6	626	4	US-10-108-260A-4299	Sequence 4299, Ap
19	954	29.6	569	4	US-10-369-493-9160	Sequence 9160, Ap
20	947	29.4	671	4	US-10-369-493-17597	Sequence 17597, A
21	929.5	28.8	588	4	US-10-369-493-15968	Sequence 15968, A
22	929.5	28.8	588	4	US-10-369-493-16330	Sequence 16330, A
23	929.5	28.8	641	4	US-10-369-493-15592	Sequence 15592, A
24	892.5	27.7	611	4	US-10-425-115-272788	Sequence 272788,
25	887.5	27.5	650	4	US-10-425-114-61058	Sequence 61058, A
26	880.5	27.3	611	4	US-10-437-963-143613	Sequence 143613,
27	880	27.3	540	4	US-10-369-493-9417	Sequence 9417, Ap
28	874	27.1	581	4	US-10-369-493-17802	Sequence 17802, A
29	800.5	24.8	724	4	US-10-275-107-67	Sequence 67, Appli
30	800	24.8	725	3	US-09-929-218-2	Sequence 2, Appli
31	800	24.8	725	4	US-10-423-543-40	Sequence 40, Appli
32	766.5	23.8	416	4	US-10-296-115-1194	Sequence 1194, Ap
33	593	18.4	363	4	US-10-767-701-42438	Sequence 42438, A
34	534	16.6	358	4	US-10-424-599-157271	Sequence 157271,
35	517	16.0	416	4	US-10-311-035-3	Sequence 3, Appli
36	401	12.4	393	4	US-10-099-322-301	Sequence 301, App
37	401	12.4	393	4	US-10-044-564-301	Sequence 301, App
38	365.5	11.3	821	4	US-10-369-493-19382	Sequence 19382, A
39	362	11.2	441	4	US-10-007-271-4	Sequence 4, Appli
40	353.5	11.0	875	4	US-10-369-493-20117	Sequence 20117, A
41	347.5	10.8	438	4	US-10-281-904-4	Sequence 4, Appli
42	345.5	10.7	799	4	US-10-425-115-205689	Sequence 205689,
43	344	10.7	694	4	US-10-087-192-1851	Sequence 1851, Ap
44	343	10.6	723	4	US-10-369-493-10942	Sequence 10942, A
45	342	10.6	1025	4	US-10-087-192-1854	Sequence 1854, Ap

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:02:46 ; Search time 5 Seconds
(without alignments)
369.778 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.....HKASMHPVTAMLVKGDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
<hr/>						
1	342	10.6	1092	1	US-10-821-234-999	Sequence 999, App
2	281.5	8.7	941	1	US-10-131-826A-464	Sequence 464, App
3	252.5	7.8	1024	1	US-10-131-826A-198	Sequence 198, App
4	93	2.9	2323	1	US-10-793-626-760	Sequence 760, App
5	91.5	2.8	406	1	US-10-131-826A-502	Sequence 502, App
6	87	2.7	903	7	US-11-057-058-65	Sequence 65, Appl
7	86.5	2.7	314	1	US-10-793-626-2552	Sequence 2552, Ap
8	85	2.6	434	1	US-10-821-234-1553	Sequence 1553, Ap
9	85	2.6	871	7	US-11-077-550-2	Sequence 2, Appli

10	85	2.6	871	7	US-11-077-550-8	Sequence 8, Appli
11	85	2.6	871	7	US-11-077-550-26	Sequence 26, Appli
12	85	2.6	871	7	US-11-077-550-153	Sequence 153, App
13	85	2.6	873	7	US-11-077-550-6	Sequence 6, Appli
14	85	2.6	873	7	US-11-077-550-149	Sequence 149, App
15	85	2.6	873	7	US-11-077-550-151	Sequence 151, App
16	85	2.6	879	7	US-11-077-550-159	Sequence 159, App
17	85	2.6	894	7	US-11-077-550-4	Sequence 4, Appli
18	85	2.6	1127	7	US-11-077-550-40	Sequence 40, Appli
19	85	2.6	1129	7	US-11-077-550-42	Sequence 42, Appli
20	84.5	2.6	944	7	US-11-057-058-68	Sequence 68, Appli
21	84	2.6	556	1	US-10-821-234-1509	Sequence 1509, Ap
22	84	2.6	3056	7	US-11-109-156-20	Sequence 20, Appli
23	83.5	2.6	1130	7	US-11-077-550-139	Sequence 139, App
24	83	2.6	966	7	US-11-057-058-67	Sequence 67, Appli
25	82.5	2.6	775	1	US-10-131-826A-120	Sequence 120, App
26	82.5	2.6	2080	1	US-10-821-234-1640	Sequence 1640, Ap
27	82	2.5	873	7	US-11-077-550-167	Sequence 167, App
28	82	2.5	875	7	US-11-077-550-10	Sequence 10, Appli
29	81.5	2.5	423	7	US-11-184-156-2	Sequence 2, Appli
30	81	2.5	877	7	US-11-077-550-157	Sequence 157, App
31	80	2.5	485	1	US-10-630-203-2	Sequence 2, Appli
32	80	2.5	485	7	US-11-103-037-1	Sequence 1, Appli
33	80	2.5	532	1	US-10-821-234-918	Sequence 918, App
34	80	2.5	1304	1	US-10-821-234-1648	Sequence 1648, Ap
35	79.5	2.5	138	1	US-10-793-626-1540	Sequence 1540, Ap
36	79.5	2.5	176	1	US-10-793-626-612	Sequence 612, App
37	79.5	2.5	878	7	US-11-077-550-12	Sequence 12, Appli
38	79.5	2.5	887	7	US-11-077-550-161	Sequence 161, App
39	79.5	2.5	907	7	US-11-077-550-16	Sequence 16, Appli
40	79.5	2.5	953	7	US-11-077-550-14	Sequence 14, Appli
41	79.5	2.5	1013	7	US-11-077-550-18	Sequence 18, Appli
42	79.5	2.5	1432	1	US-10-510-386-218	Sequence 218, App
43	79	2.4	468	7	US-11-054-385-12	Sequence 12, Appli
44	79	2.4	871	7	US-11-077-550-155	Sequence 155, App
45	79	2.4	873	7	US-11-077-550-163	Sequence 163, App

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:59:55 ; Search time 42 Seconds
(without alignments)
1397.434 Million cell updates/sec

Title: US-09-914-451-1

Perfect score: 3225

Sequence: 1 PEIVDTCSLASPASVCRTKH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62

Gapext 0.5 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB ID	
1	3225	100.0	611	1 S65947	leukotriene-A4 hyd
2	3058	94.8	611	1 JN0066	leukotriene-A4 hyd
3	3043	94.4	611	1 JC4237	leukotriene-A4 hyd
4	3042.5	94.3	610	1 S20444	leukotriene-A4 hyd
5	1464	45.4	587	2 T32546	hypothetical prote
6	1376.5	42.7	809	2 T32899	probable leukotrie
7	1206.5	37.4	612	2 T40936	probable leukotrie
8	1134.5	35.2	671	2 S61099	leukotriene-A4 hyd
9	947	29.4	671	2 D82675	aminopeptidase N X
10	668	20.7	360	2 T51870	hypothetical prote
11	388.5	12.0	785	2 S73098	aminopeptidase (EC
12	354.5	11.0	844	2 JC4054	membrane alanyl am
13	344.5	10.7	844	2 S47274	membrane alanyl am

14	341	10.6	1006	2	A59384	oxytocinase/insuli
15	341	10.6	1025	2	A59383	oxytocinase/insuli
16	340.5	10.6	916	2	I55441	vp165 - rat
17	337.5	10.5	843	2	S38364	membrane alanyl am
18	324.5	10.1	784	2	B90442	tricorn proteinase
19	317	9.8	920	2	T10052	aminopeptidase (EC
20	313.5	9.7	866	2	AI1880	aminopeptidase [im
21	310.5	9.6	988	2	T24668	hypothetical prote
22	308	9.6	964	2	G96662	probable aminopept
23	307	9.5	780	2	T37456	Tricorn proteinase
24	305.5	9.5	869	2	S76720	hypothetical prote
25	302	9.4	849	2	JC7959	lysyl aminopeptida
26	301.5	9.3	884	2	T29637	hypothetical prote
27	300	9.3	849	2	JU0191	aminopeptidase Y (
28	298.5	9.3	957	2	A47531	glutamyl aminopept
29	298.5	9.3	967	2	A30325	membrane alanyl am
30	297	9.2	472	2	A75464	probable zinc meta
31	296.5	9.2	990	2	JC8058	laeverin - human
32	291.5	9.0	848	2	B97960	membrane alanyl am
33	290.5	9.0	848	2	E95092	aminopeptidase N [
34	289	9.0	747	2	T23882	hypothetical prote
35	285	8.8	805	2	S07099	membrane alanyl am
36	284.5	8.8	882	2	T39789	aminopeptidase - f
37	281	8.7	862	2	G87094	probable aminopept
38	281	8.7	963	2	A53984	membrane alanyl am
39	279	8.7	965	2	A32852	membrane alanyl am
40	277	8.6	861	2	B70866	probable aminopept
41	275.5	8.5	844	2	S37794	aminopeptidase ysc
42	274.5	8.5	945	2	S30398	aminopeptidase N h
43	274	8.5	786	2	T23883	hypothetical prote
44	274	8.5	919	2	S42842	T16G12.2 protein -
45	273	8.5	783	2	T37457	Tricorn proteinase

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:59:39 ; Search time 231 Seconds
(without alignments)
1863.083 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.....HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	3225	100.0	610	1	LKHA4_HUMAN	P09960 homo sapien
2	3225	100.0	611	2	Q6IAT6_HUMAN	Q6iat6 homo sapien
3	3202	99.3	611	2	Q5REQ3_PONPY	Q5req3 pongo pygma
4	3090	95.8	610	1	LKHA4_CHILA	Q6s9c8 chinchilla
5	3061	94.9	610	1	LKHA4_MOUSE	P24527 mus musculu
6	3043	94.4	610	1	LKHA4_CAVPO	P19602 cavia porce
7	3042.5	94.3	609	1	LKHA4_RAT	P30349 rattus norv
8	2540.5	78.8	612	2	Q5ZJJ6_CHICK	Q5zjj6 gallus gall
9	2294.5	71.1	609	2	Q6IP81_XENLA	Q6ip81 xenopus lae
10	2284.5	70.8	609	2	Q6GL78_XENTR	Q6gl78 xenopus tro
11	2190.5	67.9	611	2	Q5RIF1_BRARE	Q5rif1 brachydanio
12	2180.5	67.6	611	2	Q6NUX4_BRARE	Q6nux4 brachydanio
13	2077.5	64.4	630	2	Q4T8V9_TETNG	Q4t8v9 tetraodon n
14	1487	46.1	625	2	O44183_CAEEL	O44183 caenorhabdi
15	1480	45.9	625	2	Q61MW9_CAEFR	Q61mw9 caenorhabdi

16	1386.5	43.0	558	2	Q7Q192_ANOGA	Q7q192 anopheles g
17	1376.5	42.7	609	2	Q44969_CAEEL	O44969 caenorhabdi
18	1369	42.4	608	2	Q86GU4_CAEEL	Q86gu4 caenorhabdi
19	1338	41.5	613	2	Q7KT44_DROME	Q7kt44 drosophila
20	1338	41.5	684	2	Q9VJ39_DROME	Q9vj39 drosophila
21	1315	40.8	606	2	Q55BR5_DICDI	Q55br5 dictyosteli
22	1212.5	37.6	614	2	Q4X265_ASPFU	Q4x265 aspergillus
23	1206.5	37.4	612	1	LKHA4_SCHPO	O94544 schizosacch
24	1199.5	37.2	647	2	Q6C3E5_YARLI	Q6c3e5 yarrowia li
25	1196.5	37.1	639	2	Q4HXX0_GIBZE	Q4hxx0 gibberella
26	1149.5	35.6	662	2	Q6CLD3_KLULA	Q6cld3 kluyveromyc
27	1145.5	35.5	652	2	Q6FTM0_CANGA	Q6ftm0 candida gla
28	1144.5	35.5	639	2	Q5B0W8_EMENI	Q5b0w8 aspergillus
29	1141	35.4	614	2	Q7S785_NEUCR	Q7s785 neurospora
30	1136	35.2	1297	2	Q4PI93_USTMA	Q4pi93 ustilago ma
31	1134.5	35.2	671	1	LKHA4 YEAST	Q10740 saccharomyc
32	1126	34.9	613	2	Q51X77_MAGGR	Q51x77 magnaporthe
33	1110	34.4	632	2	Q55RS1_CRYNE	Q55rs1 cryptococcu
34	1097.5	34.0	641	2	Q6BW21_DEBHA	Q6bw21 debaryomyce
35	1090	33.8	626	2	Q6DGD8_BRARE	Q6gdg8 brachydanio
36	1084	33.6	219	2	Q59ES1_HUMAN	Q59es1 homo sapien
37	1060.5	32.9	623	2	Q59NB8_CANAL	Q59nb8 candida alb
38	1026.5	31.8	618	2	Q6NVR0_XENTR	Q6nvr0 xenopus tro
39	1018.5	31.6	618	2	Q6GQ32_XENLA	Q6gq32 xenopus lae
40	1016.5	31.5	612	2	Q641C7_XENLA	Q641c7 xenopus lae
41	1014	31.4	650	1	AMPB_MOUSE	Q8vct3 mus musculu
42	1008.5	31.3	658	2	Q7RU04_HUMAN	Q7ru04 homo sapien
43	1006.5	31.2	650	1	AMPB_HUMAN	Q9h4a4 homo sapien
44	1005.5	31.2	286	2	Q5TZ09_BRARE	Q5tz09 brachydanio
45	1001.5	31.1	650	1	AMPB_RAT	O09175 rattus norv